



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/826,581

DATE: 01/26/2002

TIME: 16:32:24

Input Set : A:\11145-007001.txt

Output Set: N:\CRF3\01262002\I826581.raw

ENTERED

4 <110> APPLICANT: Andersson, Leif
 5 Luthman, L. Holger
 6 Marklund, Stefan
 8 <120> TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3
 SUBUNIT
 10 <130> FILE REFERENCE: 11145-007001
 12 <140> CURRENT APPLICATION NUMBER: US 09/826,581
 13 <141> CURRENT FILING DATE: 2001-04-05
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 16 <151> PRIOR FILING DATE: 2000-04-07
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 30 agattatccg gtgcgcccct tccctcccag caacccccag ccttcagggc tgtagcagct 180
 31 gagcaaatgg gggcccctcc ctctcattgc ctgacaccca atcagagaga aaccgatcct 240
 32 ggcagggcag ggtgcccggg gccgggcccc gaatagtgcg gccagccac agtgtcgca 300
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 51 tgagatggac aaggcagaag tcggtggagg aaggggagcc accagggtcag ggggaagggtg 180
 52 aggccaaggc cagttctggg gaggtggag ccaggggagt gggaaatccc agaggagcct 240
 53 ggggtctggtc tctacctcag gtccctccat aacacagagt tggacccaac cttcatcttg 300
 54 tggcctcagt ctccctacat agtagagaac aaggcactgc agtgccagag gccagcatgg 360
 55 ccaactcaga aagatgggac agagccacta cctggggcga ctctcaggtc agcccctcac 420
 56 ctgcaaatag ggccacagca tccaggcttc ccactgctgc tgtgagatga atggcgacag 480

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57 cagatgagaa cgtgctttgg aagatggagt tactgtcctc ttccctcct cccccaaca 540
58 ggtccccggt ccaggccagc tgetgagtc accgggctgg aggccacatt cccaagacc 600
59 acacccttgg ctcaagctga tctgtccggg gtgggactc caccaacagg gtgggactgc 660
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61 acggagttcc cagccacaga ggctgggag tgtgagctag aaggcctgct ggaagagagg 780
62 cctgccctgt gcctgtcccc gcaggcccca tttccaagc tgggctggga tgacgaactg 840
63 cggaaacccg gcgcccagat ctacatgcgc ttcattgcagg agcacacctg ctacgatgcc 900
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91 acagtccctt tccccagtc cactcagctc tgaactcacc tcttcattct aggcggcaca 1140
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100 catcctgact gcaactggaca tctttgtgga ccggcgtgtg tctgactgc ctgtggtcaa 1680
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113 gttgacatct gtagggtagg agcccaggca aggggggtgac taggagccat acttctctct 240
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115 gccctgaggc agaggacact atgtctggag ggagtccttt cctgccagcc ccacgagagc 360
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118 cacctggcct atccttccat ttcattgacca actcctggtg cccacactgg cctgcacctg 540
119 gtcctgtcca tggggccctt atgccagggg tccactgccaa ctgatcacct taggccgggc 600
120 acaccatccc taactggttt ctaggagacg ctctctccct cagtcattgtt gggttgtttc 660
121 ccctgattct tggcaccacac ctcagtagct gctgtagccc catggctctg cccctcact 720
122 gaacattgcy gaccacacagg tacacagget ggtgctagt gacgagaccc agcatctctt 780
123 gggcgtgggc tccctctccg acatccttca ggcactggtg ctcagccctg ctggcatcga 840
124 tgccctcggg gcctgagaag atctgagtc tcaatcccaa gccacctgca cacctggaag 900
125 ccaatgaagg gaactggaga actcagcct catcttcccc caccocctatt tgcgtgttca 960
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140 1 5 10
142 acc cct tcc tgg agc agc ctt ggg ggt tct gag cat caa gag atg agc 100
143 Thr Pro Ser Trp Ser Ser Leu Gly Gly Ser Glu His Gln Glu Met Ser
144 15 20 25
146 ttc cta gag caa gaa aac agc agc tca tgg cca tca cca gct gtg acc 148
147 Phe Leu Glu Gln Glu Asn Ser Ser Ser Trp Pro Ser Pro Ala Val Thr
148 30 35 40
150 agc agc tca gaa aga atc cgt ggg aaa cgg agg gcc aaa gcc ttg aga 196
151 Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala Leu Arg
152 45 50 55
154 tgg aca agg cag aag tgc gtg gag gaa ggg gag cca cca ggt cag ggg 244
155 Trp Thr Arg Gln Lys Ser Val Glu Glu Gly Glu Pro Pro Gly Gln Gly
156 60 65 70 75
159 gaa ggt ccc cgg tcc agg cca gct gct gag tcc acc ggg ctg gag gcc 292
160 Glu Gly Pro Arg Ser Arg Pro Ala Ala Glu Ser Thr Gly Leu Glu Ala
161 80 85 90
163 aca ttc ccc aag acc aca ccc ttg gct caa gct gat cct gcc ggg gtg 340
164 Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val
165 95 100 105
167 ggc act cca cca aca ggg tgg gac tgc ctc ccc tct gac tgt aca gcc 388
168 Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys Thr Ala
169 110 115 120
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176	Pro	Ala	Thr	Glu	Ala	Trp	Glu	Cys	Glu	Leu	Glu	Gly	Leu	Leu	Glu	Glu	
177	140					145					150					155	
179	agg	cct	gcc	ctg	tgc	ctg	tcc	ccg	cag	gcc	cca	ttt	ccc	aag	ctg	ggc	532
180	Arg	Pro	Ala	Leu	Cys	Leu	Ser	Pro	Gln	Ala	Pro	Phe	Pro	Lys	Leu	Gly	
181					160					165					170		
183	tgg	gat	gac	gaa	ctg	cgg	aaa	ccc	ggc	gcc	cag	atc	tac	atg	cgc	ttc	580
184	Trp	Asp	Asp	Glu	Leu	Arg	Lys	Pro	Gly	Ala	Gln	Ile	Tyr	Met	Arg	Phe	
185				175					180					185			
187	atg	cag	gag	cac	acc	tgc	tac	gat	gcc	atg	gca	act	agc	tcc	aag	cta	628
188	Met	Gln	Glu	His	Thr	Cys	Tyr	Asp	Ala	Met	Ala	Thr	Ser	Ser	Lys	Leu	
189			190					195					200				
191	gtc	atc	ttc	gac	acc	atg	ctg	gag	atc	aag	aag	gcc	ttc	ttt	gct	ctg	676
192	Val	Ile	Phe	Asp	Thr	Met	Leu	Glu	Ile	Lys	Lys	Ala	Phe	Phe	Ala	Leu	
193		205					210					215					
195	gtg	gcc	aac	ggt	gtg	cgg	gca	gcc	cct	cta	tgg	gac	agc	aag	aag	cag	724
196	Val	Ala	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys	Lys	Gln	
197	220					225					230					235	
199	agc	ttt	gtg	ggg	atg	ctg	acc	atc	act	gac	ttc	atc	ctg	gtg	ctg	cat	772
200	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val	Leu	His	
201					240					245					250		
203	cgc	tac	tac	agg	tcc	ccc	ctg	gtc	cag	atc	tat	gag	att	gaa	caa	cat	820
204	Arg	Tyr	Tyr	Arg	Ser	Pro	Leu	Val	Gln	Ile	Tyr	Glu	Ile	Glu	Gln	His	
205				255					260					265			
207	aag	att	gag	acc	tgg	agg	gag	atc	tac	ctg	caa	ggc	tgc	ttc	aag	cct	868
208	Lys	Ile	Glu	Thr	Trp	Arg	Glu	Ile	Tyr	Leu	Gln	Gly	Cys	Phe	Lys	Pro	
209			270					275					280				
212	ctg	gtc	tcc	atc	tct	cct	aat	gat	agc	ctg	ttt	gaa	gct	gtc	tac	acc	916
213	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val	Tyr	Thr	
214		285					290					295					
216	ctc	atc	aag	aac	cgg	atc	cat	cgc	ctg	cct	gtt	ctt	gac	ccg	gtg	tca	964
217	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro	Val	Ser	
218	300					305					310					315	
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221	Gly	Asn	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys	Phe	Leu	
222					320					325					330		
224	cac	atc	ttt	ggt	tcc	ctg	ctg	ccc	cgg	ccc	tcc	ttc	ctc	tac	cgc	act	1060
225	His	Ile	Phe	Gly	Ser	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr	Arg	Thr	
226				335					340					345			
228	atc	caa	gat	ttg	ggc	atc	ggc	aca	ttc	cga	gac	ttg	gct	gtg	gtg	ctg	1108
229	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val	Val	Leu	
230			350					355						360			
232	gag	aca	gca	ccc	atc	ctg	act	gca	ctg	gac	atc	ttt	gtg	gac	cgg	cgt	1156
233	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp	Arg	Arg	
234		365					370					375					
236	gtg	tct	gca	ctg	cct	gtg	gtc	aac	gaa	tgt	ggt	cag	gtc	gtg	ggc	ctc	1204
237	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Cys	Gly	Gln	Val	Val	Gly	Leu	

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242          400          405          410
244 cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca cta tgt      1300
245 His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr Leu Cys
246          415          420          425
248 ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg gaa gtg      1348
249 Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly Glu Val
250          430          435          440
252 atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta gtg gac      1396
253 Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu Val Asp
254          445          450          455
256 gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc ctt cag      1444
257 Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu Gln
258 460          465          470          475
260 gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc      1486
261 Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
262          480          485
265 tgagaagatc tgagtcctca atcccaagcc acctgcacac ctggaagcca atgaagggaa      1546
266 ctggagaact cagccttcac cttcccccac ccccatctgc tggttcagct atgattcagg      1606
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280          35          40          45
281 Ile Arg Gly Lys Arg Arg Ala Lys Ala Leu Arg Trp Thr Arg Gln Lys
282          50          55          60
283 Ser Val Glu Glu Gly Glu Pro Pro Gly Gln Gly Glu Gly Pro Arg Ser
284 65          70          75          80
285 Arg Pro Ala Ala Glu Ser Thr Gly Leu Glu Ala Thr Phe Pro Lys Thr
286          85          90          95
287 Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val Gly Thr Pro Pro Thr
288          100          105          110
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290          115          120          125
291 Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe Pro Ala Thr Glu Ala
292          130          135          140
293 Trp Glu Cys Glu Leu Glu Gly Leu Leu Glu Glu Arg Pro Ala Leu Cys
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VERIFICATION SUMMARY

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